

Application No.:

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/357,349B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ✓ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/357,349B

DATE: 12/26/2002

TIME: 13:24:06

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\12262002\I357349B.raw

4 <110> APPLICANT: Geerts, Hugo
 5 Masure, Stefan
 6 Cik, Miroslav
 7 Meert, Theo
 8 Ver Donk, Luc
 10 <120> TITLE OF INVENTION: Neurotrophic Growth Factor
 12 <130> FILE REFERENCE: 50936/702
 14 <140> CURRENT APPLICATION NUMBER: 09/357,349B
 15 <141> CURRENT FILING DATE: 1999-07-14
 17 <150> PRIOR APPLICATION NUMBER: 9815283.8
 18 <151> PRIOR FILING DATE: 1998-07-14
 20 <150> PRIOR APPLICATION NUMBER: 09/248,772
 21 <151> PRIOR FILING DATE: 1999-02-12
 23 <150> PRIOR APPLICATION NUMBER: 09/327,668
 24 <151> PRIOR FILING DATE: 1999-06-08
 E--> 26 <160> NUMBER OF SEQ ID NOS: 15 (see p. 2)
 28 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

OK 473 <210> SEQ ID NO: 16
 474 <211> LENGTH: 134
 475 <212> TYPE: PRT
 476 <213> ORGANISM: Homo sapiens
 480 <400> SEQUENCE: 16
 482 Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg
 E--> 483 1 5 10 15
 485 Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 E--> 486 20 25 30
 488 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 E--> 489 35 40 45
 491 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 E--> 492 50 55 60
 494 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 E--> 495 65 70 75 80
 497 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 E--> 498 85 90 95
 500 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 E--> 501 100 105 110
 503 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 E--> 504 115 120 125
 506 Lys Arg Cys Gly Cys Ile

Does Not Comply
 Corrected Diskette Needed

pp 1-4

misaligned
 amino acid
 numbers
 (see item 3
 on Error
 Summary
 sheet)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/357,349B

DATE: 12/26/2002

TIME: 13:24:06

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\12262002\I357349B.raw

E--> 507 130
 511 <210> SEQ ID NO: 17
 512 <211> LENGTH: 102
 513 <212> TYPE: PRT
 514 <213> ORGANISM: Homo sapiens
 518 <400> SEQUENCE: 17
 520 Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg
 E--> 521 1 5 10 15
 523 Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe
 E--> 524 20 25 30
 526 Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
 E--> 527 35 40 45
 529 Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
 E--> 530 50 55 60
 532 Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
 E--> 533 65 70 75 80
 535 Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 E--> 536 85 90 95
 538 Arg Glu Cys Ala Cys Val
 E--> 539 100
 543 <210> SEQ ID NO: 18
 544 <211> LENGTH: 96
 545 <212> TYPE: PRT
 546 <213> ORGANISM: Homo sapiens
 550 <400> SEQUENCE: 18
 552 Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala
 E--> 553 1 5 10 15
 555 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 E--> 556 20 25 30
 558 Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala
 E--> 559 35 40 45
 561 Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys
 E--> 562 50 55 60
 564 Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg
 E--> 565 65 70 75 80
 567 Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 E--> 568 85 90 95
 572 <210> SEQ ID NO: 19
 573 <211> LENGTH: 113
 574 <212> TYPE: PRT
 575 <213> ORGANISM: Homo sapiens
 578 <400> SEQUENCE: 19
 580 Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys
 E--> 581 1 5 10 15
 583 Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His
 E--> 584 20 25 30
 586 Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg
 E--> 587 35 40 45
 589 Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala

*same
err**same**Last sequence in submitted file**same**(see p.3)*

RAW SEQUENCE LISTING

DATE: 12/26/2002

PATENT APPLICATION: US/09/357,349B

TIME: 13:24:06

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\12262002\I357349B.raw

E--> 590 50 55 60
592 Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys
E--> 593 65 70 75 80
595 Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser
E--> 596 85 90 95
598 Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu
E--> 599 100 105 110
601 Gly
E--> 604 ①

*delete**misaligned
nos.**see p. 4 for more errors*

<110> Janssen Pharmaceutica
<120> Neurotrophic Growth Factor
<130> P50936/702
<140> US 09/357,349
<141> 1999-02-12
<160> 4
<170> PatentIn version 3.1
<210> 16
<211> 134
<212> PRT
<213> Homo sapiens

<400> 16

delete - this information
is only shown
once, at the
beginning of
file

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/357,349B

DATE: 12/26/2002
TIME: 13:24:08

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I357349B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/357,349B

DATE: 12/26/2002

TIME: 13:24:08

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF4\12262002\I357349B.raw

L:414 M:283 W: Missing Blank Line separator, <400> field identifier
 L:466 M:280 W: Numeric Identifier already exists, <110> found multiple times
 L:466 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
 L:467 M:283 W: Missing Blank Line separator, <120> field identifier
 L:467 M:280 W: Numeric Identifier already exists, <120> found multiple times
 L:467 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
 L:468 M:283 W: Missing Blank Line separator, <130> field identifier
 L:468 M:280 W: Numeric Identifier already exists, <130> found multiple times
 L:468 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
 L:469 M:283 W: Missing Blank Line separator, <140> field identifier
 L:469 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
 L:470 M:280 W: Numeric Identifier already exists, <141> found multiple times
 L:470 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
 L:470 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:471 M:280 W: Numeric Identifier already exists, <160> found multiple times
 L:471 M:281 W: Numeric Fields not Ordered, <160> not ordered!.
 L:471 M:283 W: Missing Blank Line separator, <160> field identifier
 L:472 M:280 W: Numeric Identifier already exists, <170> found multiple times
 L:473 M:283 W: Missing Blank Line separator, <210> field identifier
 L:483 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 M:332 Repeated in SeqNo=16
 L:521 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
 M:332 Repeated in SeqNo=17
 L:553 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
 M:332 Repeated in SeqNo=18
 L:581 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
 M:332 Repeated in SeqNo=19
 L:471 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (4) Counted (19)